

SEQUENCE LISTING

<110> Amano Enzyme, Inc.

<120> NOVEL PROTEIN-DEAMIDATING ENZYME, MICROORGANISM PRODUCING THE SAME, GENE ENCODING THE SAME, PRODUCTION PROCESS THEREFOR, AND USE THEREOF

<130> Q62106

<140> 09/727,769

<141> 2000-12-04

<150> JP 11-345044

<151> 1999-12-03

<160> 11

<170> PatentIn version 3.1

<210> 1

<211> 20

<212> PRT

<213> Cryseobacterium sp. No. 9670

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Gln Ile Lys Asn
20

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<213> Cryseobacterium sp. No. 9670

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Ser Pro Ser Asn Ser Tyr Leu Tyr Asp Asn Asn Leu Ile Asn Thr Asn
1 5 10 15

Cys Val Leu Thr
20

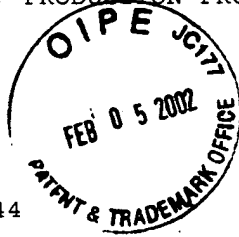
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<212> DNA

<213> Artificial Sequence

<220>



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TECH CENTER 1600/2900

31

<223> sense primer

<220>

<221> misc_feature

<222> (3)..(3)

<223> n = inosine

<220>

<221> misc_feature

<222> (6)..(6)

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<222> (9)..(9)

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<222> (15)..(15)

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B'
Cont

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ggatgttatg caagagccca taagatgaga caaatcttaa tgaacaacgg ctatgactgt 180
gaaaaacaat ttgtatacgg aaacctaaag gcatcaacag gaacttgctg tgtggcgtgg 240
agctaccacg ttgcaatatt ggtaagctat aaaaatgctt ccggagtaac ggaaaaaaga 300
attattgatc cttcactatt ttcaagcggc cctgtaacag atacagcatg gagaaacgct 360
tgcgttaaca cctcttgcgg atctgcatcc gtttctctt atgctaatac tgcaggaaat 420
gtttattaca gaagtcctag taattcttac ctgtatgaca acaatctgat caataccaac 480
tgtgtactga ctaaattttc actgctttcc ggatgttctc cttcacctgc accggatgta 540
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<213> Cryseobacterium sp. No. 9670

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Leu Ala Ser Val Ile Pro Asp Val Ala Thr Leu Asn Ser Leu Phe Asn
1 5 10 15

Gln Ile Lys Asn Gln Ser Cys Gly Thr Ser Thr Ala Ser Ser Pro Cys
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Ile Thr Phe Arg Tyr Pro Val Asp Gly Cys Tyr Ala Arg Ala His Lys
35 40 45

Met Arg Gln Ile Leu Met Asn Asn Gly Tyr Asp Cys Glu Lys Gln Phe
50 55 60

Val Tyr Gly Asn Leu Lys Ala Ser Thr Gly Thr Cys Cys Val Ala Trp
65 70 75 80

Ser Tyr His Val Ala Ile Leu Val Ser Tyr Lys Asn Ala Ser Gly Val
85 90 95

Thr Glu Lys Arg Ile Ile Asp Pro Ser Leu Phe Ser Ser Gly Pro Val
 100 105 110

Thr Asp Thr Ala Trp Arg Asn Ala Cys Val Asn Thr Ser Cys Gly Ser
 115 120 125

Ala Ser Val Ser Ser Tyr Ala Asn Thr Ala Gly Asn Val Tyr Tyr Arg
 130 135 140

Ser Pro Ser Asn Ser Tyr Leu Tyr Asp Asn Asn Leu Ile Asn Thr Asn
 145 150 155 160

Cys Val Leu Thr Lys Phe Ser Leu Leu Ser Gly Cys Ser Pro Ser Pro
 165 170 175

Ala Pro Asp Val Ser Ser Cys Gly Phe
 180 185

<210> 7
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atg aaa aat ctt ttt tta tca atg atg gcc ttt gtg acc gtc tta 105
 Met Lys Asn Leu Phe Leu Ser Met Met Ala Phe Val Thr Val Leu
 -135 -130 -125

act ttt aat tcc tgt gcc gat tcc aac ggg aat cag gaa atc aac 150
 Thr Phe Asn Ser Cys Ala Asp Ser Asn Gly Asn Gln Glu Ile Asn
 -120 -115 -110

gga aag gaa aaa cta agt gta aat gat tct aag ctg aaa gat ttc gga 198

B1
Cont.

Gly	Lys	Glu	Lys	Leu	Ser	Val	Asn	Asp	Ser	Lys	Leu	Lys	Asp	Phe	Gly		
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aag	act	gta	ccg	gta	ggg	ata	gac	gaa	gaa	aac	gga	atg	ata	aag	gtg		246
Lys	Thr	Val	Pro	Val	Gly	Ile	Asp	Glu	Glu	Asn	Gly	Met	Ile	Lys	Val		
				-85				-80					-75				
tca	ttt	atg	tta	act	gcg	caa	ttc	tat	gaa	att	aag	ccg	acc	aaa	gaa		294
Ser	Phe	Met	Leu	Thr	Ala	Gln	Phe	Tyr	Glu	Ile	Lys	Pro	Thr	Lys	Glu		
			-70					-65					-60				
aat	gag	cag	tat	atc	gga	atg	ctt	aga	cag	gct	gtt	aag	aat	gaa	tct		342
Asn	Glu	Gln	Tyr	Ile	Gly	Met	Leu	Arg	Gln	Ala	Val	Lys	Asn	Glu	Ser		
	-55					-50						-45					
cct	gta	cac	att	ttc	tta	aag	cct	aat	agc	aat	gaa	ata	gga	aaa	gtg		390
Pro	Val	His	Ile	Phe	Leu	Lys	Pro	Asn	Ser	Asn	Glu	Ile	Gly	Lys	Val		
	-40					-35					-30						
gag	tct	gca	agt	ccg	gaa	gac	gta	aga	tat	ttt	aaa	acg	atc	ctg	aca		438
Glu	Ser	Ala	Ser	Pro	Glu	Asp	Val	Arg	Tyr	Phe	Lys	Thr	Ile	Leu	Thr		
	-25				-20				-15					-10			
aaa	gaa	gta	aaa	ggg	caa	acc	aat	aaa	ttg	gcg	agt	gta	att	cct	gat		486
Lys	Glu	Val	Lys	Gly	Gln	Thr	Asn	Lys	Leu	Ala	Ser	Val	Ile	Pro	Asp		
			-5				-1	1				5					
gta	gct	aca	tta	aat	tct	tta	ttc	aat	caa	ata	aag	aat	cag	tct	tgc		534
Val	Ala	Thr	Leu	Asn	Ser	Leu	Phe	Asn	Gln	Ile	Lys	Asn	Gln	Ser	Cys		
		10					15					20					
ggg	acc	tct	acg	gcg	tcc	tca	cca	tgc	atc	aca	ttc	aga	tat	cct	gta		582
Gly	Thr	Ser	Thr	Ala	Ser	Ser	Pro	Cys	Ile	Thr	Phe	Arg	Tyr	Pro	Val		
	25					30					35						
gac	gga	tgt	tat	gca	aga	gcc	cat	aag	atg	aga	caa	atc	tta	atg	aac		630
Asp	Gly	Cys	Tyr	Ala	Arg	Ala	His	Lys	Met	Arg	Gln	Ile	Leu	Met	Asn		
	40				45				50					55			
aac	ggc	tat	gac	tgt	gaa	aaa	caa	ttt	gta	tac	gga	aac	cta	aag	gca		678
Asn	Gly	Tyr	Asp	Cys	Glu	Lys	Gln	Phe	Val	Tyr	Gly	Asn	Leu	Lys	Ala		
			60					65					70				
tca	aca	gga	act	tgc	tgt	gtg	gcg	tgg	agc	tac	cac	gtt	gca	ata	ttg		726
Ser	Thr	Gly	Thr	Cys	Cys	Val	Ala	Trp	Ser	Tyr	His	Val	Ala	Ile	Leu		
			75					80					85				
gta	agc	tat	aaa	aat	gct	tcc	gga	gta	acg	gaa	aaa	aga	att	att	gat		774
Val	Ser	Tyr	Lys	Asn	Ala	Ser	Gly	Val	Thr	Glu	Lys	Arg	Ile	Ile	Asp		
		90				95						100					
cct	tca	cta	ttt	tca	agc	ggg	cct	gta	aca	gat	aca	gca	tgg	aga	aac		822
Pro	Ser	Leu	Phe	Ser	Ser	Gly	Pro	Val	Thr	Asp	Thr	Ala	Trp	Arg	Asn		
		105				110					115						

B1
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gct tgc gtt aac acb tct tgc gga tct gca tcc gtt tcc tct tat gct 870
 Ala Cys Val Asn Thr Ser Cys Gly Ser Ala Ser Val Ser Ser Tyr Ala
 120 125 130 135

aat act gca gga aat gtt tat tac aga agt cct agt aat tct tac ctg 918
 Asn Thr Ala Gly Asn Val Tyr Tyr Arg Ser Pro Ser Asn Ser Tyr Leu
 140 145 150

tat gac aac aat ctg atc aat acc aac tgt gta ctg act aaa ttt tca 966
 Tyr Asp Asn Asn Leu Ile Asn Thr Asn Cys Val Leu Thr Lys Phe Ser
 155 160 165

ctg ctt tcc gga tgt tct cct tca cct gca ccg gat gta tcc agc tgt 1014
 Leu Leu Ser Gly Cys Ser Pro Ser Pro Ala Pro Asp Val Ser Ser Cys
 170 175 180

gga ttt taattaattg ataattttac agcacctgct catttacaga atcagcaggt 1070
 Gly Phe
 185

gctgttatat 1080

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 <212> PRT
 <213> Cryseobacterium sp. No. 9670

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 -135 -130 -125

Thr Phe Asn Ser Cys Ala Asp Ser Asn Gly Asn Gln Glu Ile Asn
 -120 -115 -110

Gly Lys Glu Lys Leu Ser Val Asn Asp Ser Lys Leu Lys Asp Phe Gly
 -105 -100 -95 -90

Lys Thr Val Pro Val Gly Ile Asp Glu Glu Asn Gly Met Ile Lys Val
 -85 -80 -75

Ser Phe Met Leu Thr Ala Gln Phe Tyr Glu Ile Lys Pro Thr Lys Glu
 -70 -65 -60

Asn Glu Gln Tyr Ile Gly Met Leu Arg Gln Ala Val Lys Asn Glu Ser
 -55 -50 -45

Pro Val His Ile Phe Leu Lys Pro Asn Ser Asn Glu Ile Gly Lys Val

B1
 Cont.

-40

-35

-30

Glu Ser Ala Ser Pro Glu Asp Val Arg Tyr Phe Lys Thr Ile Leu Thr
-25 -20 -15 -10

Lys Glu Val Lys Gly Gln Thr Asn Lys Leu Ala Ser Val Ile Pro Asp
-5 -1 1 5

Val Ala Thr Leu Asn Ser Leu Phe Asn Gln Ile Lys Asn Gln Ser Cys
10 15 20

Gly Thr Ser Thr Ala Ser Ser Pro Cys Ile Thr Phe Arg Tyr Pro Val
25 30 35

Asp Gly Cys Tyr Ala Arg Ala His Lys Met Arg Gln Ile Leu Met Asn
40 45 50 55

Asn Gly Tyr Asp Cys Glu Lys Gln Phe Val Tyr Gly Asn Leu Lys Ala
60 65 70

Ser Thr Gly Thr Cys Cys Val Ala Trp Ser Tyr His Val Ala Ile Leu
75 80 85

Val Ser Tyr Lys Asn Ala Ser Gly Val Thr Glu Lys Arg Ile Ile Asp
90 95 100

Pro Ser Leu Phe Ser Ser Gly Pro Val Thr Asp Thr Ala Trp Arg Asn
105 110 115

Ala Cys Val Asn Thr Ser Cys Gly Ser Ala Ser Val Ser Ser Tyr Ala
120 125 130 135

Asn Thr Ala Gly Asn Val Tyr Tyr Arg Ser Pro Ser Asn Ser Tyr Leu
140 145 150

Tyr Asp Asn Asn Leu Ile Asn Thr Asn Cys Val Leu Thr Lys Phe Ser
155 160 165

Leu Leu Ser Gly Cys Ser Pro Ser Pro Ala Pro Asp Val Ser Ser Cys
170 175 180

Gly Phe
185

<210> 9
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<212> DNA
<213> Artificial Sequence

<220>
<223> sense primer

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ccgaattctt ggcgagtgtg attcctgatg 30

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<212> DNA
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<223> sense primer

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<210> 11
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<212> DNA
<213> Artificial Sequence

<220>
<223> anti-sense primer

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tcgaattctt aaaatccaca gctggatac 29

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